OIPE

RAW SEQUENCE LISTING DATE: 01/27/2002
PATENT APPLICATION: US/10/039,073 TIME: 15:30:11

Input Set : A:\SEQLIST.txt
Output Set: N:\CRF3\01272002\J039073.raw

ENTERED

```
 4 <110> APPLICANT: Kapeller-Libermann, Rosana
 5         Williamson, Mark
 7 <120> TITLE OF INVENTION: 17867, A Novel Human Aminopeptidase
10 <130> FILE REFERENCE: 35800/240749(5800-36
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C--> 12 **<140> CURRENT APPLICATION NUMBER: US/10/039,073**
C--> 12 **<141> CURRENT FILING DATE: 2001-12-31**
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12 <150> PRIOR APPLICATION NUMBER: 09/345,650
13 <151> PRIOR FILING DATE: 1999-06-30
15 <160> NUMBER OF SEQ ID NOS: 3
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 960
21 <212> TYPE: PRT
22 <213> ORGANISM: Homo sapiens
24 <400> SEQUENCE: 1
25 Met Phe His Ser Ser Ala Met Val Asn Ser His Arg Lys Pro Met Phe
26  1               5                   10                  15
27 Asn Ile His Arg Gly Phe Tyr Cys Leu Thr Ala Ile Leu Pro Gln Ile
28              20                  25                  30
29 Cys Ile Cys Ser Gln Phe Ser Val Pro Ser Ser Tyr His Phe Thr Glu
30              35                  40                  45
31 Asp Pro Gly Ala Phe Pro Val Ala Thr Asn Gly Glu Arg Phe Pro Trp
32 ·    50                  55                  60
33 Gln Glu Leu Arg Leu Pro Ser Val Val Ile Pro Leu His Tyr Asp Leu
34 65                  70                  75                  80
35 Phe Val His Pro Asn Leu Thr Ser Leu Asp Phe Val Ala Ser Glu Lys
36              85                  90                  95
37 Ile Glu Val Leu Val Ser Asn Ala Thr Gln Phe Ile Ile Leu His Ser
38              100                 105                 110
39 Lys Asp Leu Glu Ile Thr Asn Ala Thr Leu Gln Ser Glu Glu Asp Ser
40              115                 120                 125
41 Arg Tyr Met Lys Pro Gly Lys Glu Leu Lys Val Leu Ser Tyr Pro Ala
42       130                 135                 140
43 His Glu Gln Ile Ala Leu Leu Val Pro Glu Lys Leu Thr Pro His Leu
44 145                 150                 155                 160
45 Lys Tyr Tyr Val Ala Met Asp Phe Gln Ala Lys Leu Gly Asp Gly Phe
46              165                 170                 175
47 Glu Gly Phe Tyr Lys Ser Thr Tyr Arg Thr Leu Gly Gly Glu Thr Arg
48              180                 185                 190
49 Ile Leu Ala Val Thr Asp Phe Glu Pro Thr Gln Ala Arg Met Ala Phe
50              195                 200                 205
51 Pro Cys Phe Asp Glu Pro Leu Phe Lys Ala Asn Phe Ser Ile Lys Ile
52       210                 215                 220
```

```
 53 Arg Arg Glu Ser Arg His Ile Ala Leu Ser Asn Met Pro Lys Val Lys
 54 225             230             235         240
 55 Thr Ile Glu Leu Glu Gly Gly Leu Leu Glu Asp His Phe Glu Thr Thr
 56             245             250             255
 57 Val Lys Met Ser Thr Tyr Leu Val Ala Tyr Ile Val Cys Asp Phe His
 58         260             265             270
 59 Ser Leu Ser Gly Phe Thr Ser Ser Gly Val Lys Val Ser Ile Tyr Ala
 60         275             280             285
 61 Ser Pro Asp Lys Arg Asn Gln Thr His Tyr Ala Leu Gln Ala Ser Leu
 62     290             295             300
 63 Lys Leu Leu Asp Phe Tyr Glu Lys Tyr Phe Asp Ile Tyr Tyr Pro Leu
 64 305             310             315             320
 65 Ser Lys Leu Asp Leu Ile Ala Ile Pro Asp Phe Ala Pro Gly Ala Met
 66             325             330             335
 67 Glu Asn Trp Gly Leu Ile Thr Tyr Arg Glu Thr Ser Leu Leu Phe Asp
 68             340             345             350
 69 Pro Lys Thr Ser Ser Ala Ser Asp Lys Leu Trp Val Thr Arg Val Ile
 70         355             360             365
 71 Ala His Glu Leu Ala His Gln Trp Phe Gly Asn Leu Val Thr Met Glu
 72     370             375             380
 73 Trp Trp Asn Asp Ile Trp Leu Lys Glu Gly Phe Ala Lys Tyr Met Glu
 74 385             390             395             400
 75 Leu Ile Ala Val Asn Ala Thr Tyr Pro Glu Leu Gln Phe Asp Asp Tyr
 76             405             410             415
 77 Phe Leu Asn Val Cys Phe Glu Val Ile Thr Lys Asp Ser Leu Asn Ser
 78             420             425             430
 79 Ser Arg Pro Ile Ser Lys Pro Ala Glu Thr Pro Thr Gln Ile Gln Glu
 80         435             440             445
 81 Met Phe Asp Glu Val Ser Tyr Asn Lys Gly Ala Cys Ile Leu Asn Met
 82     450             455             460
 83 Leu Lys Asp Phe Leu Gly Glu Glu Lys Phe Gln Lys Gly Ile Ile Gln
 84 465             470             475             480
 85 Tyr Leu Lys Lys Phe Ser Tyr Arg Asn Ala Lys Asn Asp Asp Leu Trp
 86             485             490             495
 87 Ser Ser Leu Ser Asn Ser Cys Leu Glu Ser Asp Phe Thr Ser Gly Gly
 88             500             505             510
 89 Val Cys His Ser Asp Pro Lys Met Thr Ser Asn Met Leu Ala Phe Leu
 90         515             520             525
 91 Gly Glu Asn Ala Glu Val Lys Glu Met Met Thr Thr Trp Thr Leu Gln
 92     530             535             540
 93 Lys Gly Ile Pro Leu Leu Val Val Lys Gln Asp Gly Cys Ser Leu Arg
 94 545             550             555             560
 95 Leu Gln Gln Glu Arg Phe Leu Gln Gly Val Phe Gln Glu Asp Pro Glu
 96             565             570             575
 97 Trp Arg Ala Leu Gln Glu Arg Tyr Leu Trp His Ile Pro Leu Thr Tyr
 98             580             585             590
 99 Ser Thr Ser Ser Ser Asn Val Ile His Arg His Ile Leu Lys Ser Lys
100             595             600             605
101 Thr Asp Thr Leu Asp Leu Pro Glu Lys Thr Ser Trp Val Lys Phe Asn
```

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```
102     610                 615              620
103 Val Asp Ser Asn Gly Tyr Tyr Ile Val His Tyr Glu Gly His Gly Trp
104 625                 630              635              640
105 Asp Gln Leu Ile Thr Gln Leu Asn Gln Asn His Thr Leu Leu Arg Pro
106                 645              650              655
107 Lys Asp Arg Val Gly Leu Ile His Asp Val Phe Gln Leu Val Gly Ala
108                 660              665              670
109 Gly Arg Leu Thr Leu Asp Lys Ala Leu Asp Met Thr Tyr Tyr Leu Gln
110             675              680              685
111 His Glu Thr Ser Ser Pro Ala Leu Leu Glu Gly Leu Ser Tyr Leu Glu
112         690              695              700
113 Ser Phe Tyr His Met Met Asp Arg Arg Asn Ile Ser Asp Ile Ser Glu
114 705                 710              715              720
115 Asn Leu Lys Arg Tyr Leu Leu Gln Tyr Phe Lys Pro Val Ile Asp Arg
116                 725              730              735
117 Gln Ser Trp Ser Asp Lys Gly Ser Val Trp Asp Arg Met Leu Arg Ser
118             740              745              750
119 Ala Leu Leu Lys Leu Ala Cys Asp Leu Asn His Ala Pro Cys Ile Gln
120         755              760              765
121 Lys Ala Ala Glu Leu Phe Ser Gln Trp Met Glu Ser Ser Gly Lys Leu
122     770              775              780
123 Asn Ile Pro Thr Asp Val Leu Lys Ile Val Tyr Ser Val Gly Ala Gln
124 785                 790              795              800
125 Thr Thr Ala Gly Trp Asn Tyr Leu Leu Glu Gln Tyr Glu Leu Ser Met
126                 805              810              815
127 Ser Ser Ala Glu Gln Asn Lys Ile Leu Tyr Ala Leu Ser Thr Ser Lys
128             820              825              830
129 His Gln Glu Lys Leu Leu Lys Leu Ile Glu Leu Gly Met Glu Gly Lys
130         835              840              845
131 Val Ile Lys Thr Gln Asn Leu Ala Ala Leu Leu His Ala Ile Ala Arg
132     850              855              860
133 Arg Pro Lys Gly Gln Gln Leu Ala Trp Asp Phe Val Arg Glu Asn Trp
134 865                 870              875              880
135 Thr His Leu Leu Lys Lys Phe Asp Leu Gly Ser Tyr Asp Ile Arg Met
136                 885              890              895
137 Ile Ile Ser Gly Thr Thr Ala His Phe Ser Ser Lys Asp Lys Leu Gln
138             900              905              910
139 Glu Val Lys Leu Phe Phe Glu Ser Leu Glu Ala Gln Gly Ser His Leu
140         915              920              925
141 Asp Ile Phe Gln Thr Val Leu Glu Thr Ile Thr Lys Asn Ile Lys Trp
142     930              935              940
143 Leu Glu Lys Asn Leu Pro Thr Leu Arg Thr Trp Leu Met Val Asn Thr
144 945                 950              955              960
147 <210> SEQ ID NO: 2
148 <211> LENGTH: 3366
149 <212> TYPE: DNA
150 <213> ORGANISM: Homo sapiens
152 <220> FEATURE:
153 <221> NAME/KEY: CDS
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154 <222> LOCATION: (146)...(3028)
156 <400> SEQUENCE: 2
157 ccccgcgtcc ggcatgattt aagattaaat tcatgtattg aaaatattgt tcagacccca 60
158 tgtgacataa ctggagccag tgcagtgcca tgaagaacta cgagattagc ctggatatta 120
159 acttgtcttc tagagaatag atttc atg ttc cat tct tct gca atg gtt aat   172
160                              Met Phe His Ser Ser Ala Met Val Asn
161                               1               5
163 tca cac aga aaa cca atg ttt aac att cac aga gga ttt tac tgc tta   220
164 Ser His Arg Lys Pro Met Phe Asn Ile His Arg Gly Phe Tyr Cys Leu
165   10              15                  20                  25
167 aca gcc atc ttg ccc caa ata tgc att tgt tct cag ttc tca gtg cca   268
168 Thr Ala Ile Leu Pro Gln Ile Cys Ile Cys Ser Gln Phe Ser Val Pro
169              30                  35                  40
171 tct agt tat cac ttc act gag gat cct ggg gct ttc cca gta gcc act   316
172 Ser Ser Tyr His Phe Thr Glu Asp Pro Gly Ala Phe Pro Val Ala Thr
173              45                  50                  55
175 aat ggg gaa cga ttt cct tgg cag gag cta agg ctc ccc agt gtg gtc   364
176 Asn Gly Glu Arg Phe Pro Trp Gln Glu Leu Arg Leu Pro Ser Val Val
177          60                  65                  70
179 att cct ctc cat tat gac ctc ttt gtc cac ccc aat ctc acc tct ctg   412
180 Ile Pro Leu His Tyr Asp Leu Phe Val His Pro Asn Leu Thr Ser Leu
181       75                  80                  85
183 gac ttt gtt gca tct gag aag atc gaa gtc ttg gtc agc aat gct acc   460
184 Asp Phe Val Ala Ser Glu Lys Ile Glu Val Leu Val Ser Asn Ala Thr
185   90              95                  100                 105
187 cag ttt atc atc ttg cac agc aaa gat ctt gaa atc acg aat gcc acc   508
188 Gln Phe Ile Ile Leu His Ser Lys Asp Leu Glu Ile Thr Asn Ala Thr
189              110                 115                 120
191 ctt cag tca gag gaa gat tca aga tac atg aaa cca gga aaa gaa ctg   556
192 Leu Gln Ser Glu Glu Asp Ser Arg Tyr Met Lys Pro Gly Lys Glu Leu
193              125                 130                 135
195 aaa gtt ttg agt tac cct gct cat gaa caa att gca ctg ctg gtt cca   604
196 Lys Val Leu Ser Tyr Pro Ala His Glu Gln Ile Ala Leu Leu Val Pro
197          140                 145                 150
199 gag aaa ctt acg cct cac ctg aaa tac tat gtg gct atg gac ttc caa   652
200 Glu Lys Leu Thr Pro His Leu Lys Tyr Tyr Val Ala Met Asp Phe Gln
201       155                 160                 165
203 gcc aag tta ggt gat ggc ttt gaa ggg ttt tat aaa agc aca tac aga   700
204 Ala Lys Leu Gly Asp Gly Phe Glu Gly Phe Tyr Lys Ser Thr Tyr Arg
205 170                 175                 180                 185
207 act ctt ggt ggt gaa aca aga att ctt gca gta aca gat ttt gag cca   748
208 Thr Leu Gly Gly Glu Thr Arg Ile Leu Ala Val Thr Asp Phe Glu Pro
209              190                 195                 200
211 acc cag gca cgc atg gct ttc cct tgc ttt gat gaa ccg ttg ttc aaa   796
212 Thr Gln Ala Arg Met Ala Phe Pro Cys Phe Asp Glu Pro Leu Phe Lys
213              205                 210                 215
215 gcc aac ttt tca atc aag ata cga aga gag agc agg cat att gca cta   844
216 Ala Asn Phe Ser Ile Lys Ile Arg Arg Glu Ser Arg His Ile Ala Leu
217              220                 225                 230
```

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```
219 tcc aac atg cca aag gtt aag aca att gaa ctt gaa gga ggt ctt ttg    892
220 Ser Asn Met Pro Lys Val Lys Thr Ile Glu Leu Glu Gly Gly Leu Leu
221     235             240             245
223 gaa gat cac ttt gaa act act gta aaa atg agt aca tac ctt gta gcc    940
224 Glu Asp His Phe Glu Thr Thr Val Lys Met Ser Thr Tyr Leu Val Ala
225 250             255             260             265
227 tac ata gtt tgt gat ttc cac tct ctg agt ggc ttc act tca tca ggg    988
228 Tyr Ile Val Cys Asp Phe His Ser Leu Ser Gly Phe Thr Ser Ser Gly
229             270             275             280
231 gtc aag gtg tcc atc tat gca tcc cca gac aaa cgg aat caa aca cat    1036
232 Val Lys Val Ser Ile Tyr Ala Ser Pro Asp Lys Arg Asn Gln Thr His
233             285             290             295
235 tat gct ttg cag gca tca ctg aag cta ctt gat ttt tat gaa aag tac    1084
236 Tyr Ala Leu Gln Ala Ser Leu Lys Leu Leu Asp Phe Tyr Glu Lys Tyr
237         300             305             310
239 ttt gat atc tac tat cca ctc tcc aaa ctg gat tta att gct att cct    1132
240 Phe Asp Ile Tyr Tyr Pro Leu Ser Lys Leu Asp Leu Ile Ala Ile Pro
241     315             320             325
243 gac ttt gca cct gga gcc atg gaa aat tgg ggc ctc att aca tat agg    1180
244 Asp Phe Ala Pro Gly Ala Met Glu Asn Trp Gly Leu Ile Thr Tyr Arg
245 330             335             340             345
247 gag acg tca ctg ctt ttt gac ccc aag acc tct tct gct tcc gat aaa    1228
248 Glu Thr Ser Leu Leu Phe Asp Pro Lys Thr Ser Ser Ala Ser Asp Lys
249             350             355             360
251 ctg tgg gtc acc aga gtc ata gcc cat gaa ctg gcg cac cag tgg ttt    1276
252 Leu Trp Val Thr Arg Val Ile Ala His Glu Leu Ala His Gln Trp Phe
253             365             370             375
255 ggc aac ctg gtc aca atg gaa tgg tgg aat gat att tgg ctt aag gag    1324
256 Gly Asn Leu Val Thr Met Glu Trp Trp Asn Asp Ile Trp Leu Lys Glu
257     380             385             390
259 ggt ttt gca aaa tac atg gaa ctt atc gct gtt aat gct aca tat cca    1372
260 Gly Phe Ala Lys Tyr Met Glu Leu Ile Ala Val Asn Ala Thr Tyr Pro
261     395             400             405
263 gag ctg caa ttt gat gac tat ttt ttg aat gtg tgt ttt gaa gta att    1420
264 Glu Leu Gln Phe Asp Asp Tyr Phe Leu Asn Val Cys Phe Glu Val Ile
265 410             415             420             425
267 aca aaa gat tca ttg aat tca tcc cgc cct atc tcc aaa cca gcg gaa    1468
268 Thr Lys Asp Ser Leu Asn Ser Ser Arg Pro Ile Ser Lys Pro Ala Glu
269             430             435             440
271 acc ccg act caa ata cag gaa atg ttt gat gaa gtt tcc tat aac aag    1516
272 Thr Pro Thr Gln Ile Gln Glu Met Phe Asp Glu Val Ser Tyr Asn Lys
273             445             450             455
275 gga gct tgt att ttg aat atg ctc aag gat ttt ctg ggt gag gag aaa    1564
276 Gly Ala Cys Ile Leu Asn Met Leu Lys Asp Phe Leu Gly Glu Glu Lys
277     460             465             470
279 ttc cag aaa gga ata att cag tac tta aag aag ttc agc tat aga aat    1612
280 Phe Gln Lys Gly Ile Ile Gln Tyr Leu Lys Lys Phe Ser Tyr Arg Asn
281     475             480             485
283 gct aag aat gat gac ttg tgg agc agt ctg tca aat agt tgt tta gaa    1660
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VERIFICATION SUMMARY   DATE: 01/27/2002
PATENT APPLICATION: **US/10/039,073**   TIME: 15:30:12

Input Set : **A:\SEQLIST.txt**
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date